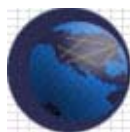




Integrative Cancer Research Special Interest Group Teleconference

Genome Annotation SIG Meeting Minutes

Date, Time & Location:	July 1, 2004 3:00 – 4:00 EDT
Attendees:	Cathy Wu – Georgetown Rakesh Nagarajan – Wash U Harold Riethman – Wistar Lincoln Stein – Cold Spring Harbor Terry Disz - U of C Ross Overbeek – U of C Jay Lewis – U of C Kutbuddin Doctor – Burnham Edith Zang – Institute for Cancer Prevention Naveen Vinukanda – Institute for Cancer Prevention Vincent Yau – Oregon Health David Kane – SRA/NCI Juli Klemm - BAH
Application Presentations	<p><u>SEED</u></p> <p>Ross Overbeek and Terry Disz gave a presentation of SEED. The slides can be downloaded from http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/gene_annotation</p> <p><u>SEED Q & A</u></p> <p>Cathy Wu: What is the source of the annotations?</p> <ul style="list-style-type: none">- Most of the annotations are predicted. SEED provides an environment for an expert to be able to clean up these annotations. <p>Lincoln Stein: Could SEED be used for community annotation?</p> <ul style="list-style-type: none">- SEED was not specifically designed for this but it is possible.- Goal with current SEED project is to “annotate 1000 genomes accurately” by annotating subsystems. It is envisioned that a few could be done manually, then the rest would be automated <p>Lincoln Stein: Most of the vertebrate annotation work involves annotation of genomes horizontally, rather than vertically. This vertical approach makes good sense.</p> <p>Cathy Wu: SEED is a tremendous tool that could be of great use to the UniProt consortium.</p> <p>Kutbuddin Doctor: Can one use SEED to combine personal annotations with public annotations?</p> <ul style="list-style-type: none">- Any user can develop their own subsystem. SEED has the concept of “non-master” assignments.- Most people run the SEED on their own laptop, then exchange annotations with one another. <p><u>Generic Genome Browser</u></p> <p>Lincoln Stein gave a presentation of GBrowse. The slides can be downloaded</p>



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from

http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/gene_annotation

GBrowse Q&A

Rakesh Nagarajan: Can GBrowse be use to view 2 overlaid genomes?

- Iowa State has made some modifications to GBrowse to add an alignment track for joining genomes. This modification will be released soon.

How are new tracks shared?

- In general, the entire track is shared. There are some workarounds that allow sharing of individual features of a track.
- There is a security built into GBrowse that allows tracks to be password protected.

Juli: What relational db adapters exist for GBrowse?

- Three have been written. A user wanting to bring in a new relational data source would need to modify one of these.
 - o A lightweight and generic adapter based on a simple 4-table database. Useful for people starting from scratch
 - o The main GMOD adapter written for Postgrs. Rich, ontology-based schema.
 - o BioSQL, shared with BioPerl, BioJava, BioPython

Cathy Wu: How are gene objects related to protein objects?

- GBrowse is not intended to make such assignments but rather to point at the smart database containing this information.

Simon Lin: How is the performance? Is most of the work performed on the server?

- Yes, all work is server-side.

Other Items Discussed

- The next Genome Annotation SIG meeting will be Thursday, August 5, at 3:00pm ET.
- Function Express and GOMiner will be presented at the next meeting.

Action Items:

Name Responsible	Action Item	Date Due	Notes
Juli Klemm	Distribute meeting minutes	7/6/04	
Juli Klemm	Post presentations on the caBIG forum	7/6/04	
All participants	Send Juli preferred dates for ICR face-to-face meeting	7/9/04	